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OM protein - protein search, using sw model

Run on: January 24, 2003, 17:26:51 ; Search time 35 Seconds

(without alignments)
2761.031 Million cell updates/sec

Title: US-09-894-657-5

Perfect score: 2416
Sequence: 1 MDVENEQILNVNPPADPNLS.....RGRKRFVSEGDRGLKPESEY 469

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 671580 seqs, 206047115 residues

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL_21:*

- 1: sp-archaea:*
- 2: sp-bacteria:*
- 3: sp-fungi:*
- 4: sp-human:*
- 5: sp-invertebrate:*
- 6: sp-mammal:*
- 7: sp-mhc:*
- 8: sp-organelle:*
- 9: sp-phage:*
- 10: sp-plant:*
- 11: sp-rodent:*
- 12: sp-virus:*
- 13: sp-vertebrate:*
- 14: sp-unclassified:*
- 15: sp-virus:*
- 16: sp-bacteriap:*
- 17: sp-archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2410	99.8	469	4 O8TR5	O8TR5 homo sapien
2	2391	99.0	469	4 O1501	O1501 homo sapien
3	2361	97.7	469	11 O61823	O61823 mus musculu
4	2356	97.5	469	11 P97296	P97296 mus musculu
5	2332	96.5	458	4 O99834	O99834 homo sapien
6	2314	95.8	469	11 O9101	O9101 rattus norv
7	2078	86.0	467	13 O8RTX3	O8RTX3 gallus gall
8	859	33.6	463	5 O96944	O96944 suberites d
9	773	32.0	507	5 O9VY91	O9VY91 drosophila
10	438.5	18.1	702	10 O94BR1	O94BR1 arabidopsis
11	419	17.3	729	10 O9FMK4	O9FMK4 arabidopsis
12	386	16.0	693	10 O80548	O80548 arabidopsis
13	369	15.3	702	10 O8W404	O8W404 arabidopsis
14	369	15.3	942	10 O9S2X0	O9S2X0 arabidopsis
15	364	15.1	618	10 O64378	O64378 arabidopsis
16	358.5	14.8	633	10 O9STL9	O9STL9 arabidopsis

17	137	5.7	787	10 O41583	O41583 tritium ae
18	135.5	5.6	1401	10 O9LQ7	O9LQ7 arabidopsis
19	130	5.4	747	10 O82233	O82233 arabidopsis
20	130	5.4	747	10 O8W414	O8W414 arabidopsis
21	129	5.3	355	10 O23523	O23523 arabidopsis
22	129	5.3	1606	10 O9LX39	O9LX39 arabidopsis
23	126.5	5.2	645	4 O96165	O96165 homo sapien
24	126.5	5.2	1560	4 O43177	O43177 homo sapien
25	123	5.1	657	10 O9S538	O9S538 arabidopsis
26	122.5	5.1	907	4 P78344	P78344 homo sapien
27	122	5.0	726	10 O9LTY1	O9LTY1 arabidopsis
28	121	5.0	907	6 P79398	P79398 oryctolagus
29	121	5.0	1004	2 O93617	O93617 rickettsia
30	119	4.9	1287	4 O92549	O92549 homo sapien
31	119	4.9	1824	5 O9NBH3	O9NBH3 strongyloce
32	117.5	4.9	263	10 O9S0H8	O9S0H8 arabidopsis
33	117	4.8	136	6 O95146	O95146 bos taurus
34	117	4.8	351	17 O980F5	O980F5 sulfolobus
35	116.5	4.8	652	3 O75011	O75011 schizosacch
36	116	4.8	478	2 O9AJL4	O9AJL4 marine cfb-
37	115.5	4.8	751	10 O9FUM7	O9FUM7 arabidopsis
38	115.5	4.8	780	10 O932T6	O932T6 arabidopsis
39	115	4.8	567	5 O9NBH2	O9NBH2 strongyloce
40	114.5	4.7	689	4 O15597	O15597 homo sapien
41	114.5	4.7	1585	4 O43432	O43432 homo sapien
42	113.5	4.7	1453	10 O9C6F9	O9C6F9 arabidopsis
43	112.5	4.7	1251	4 O8TE62	O8TE62 homo sapien
44	112.5	4.7	1563	4 O8TR61	O8TR61 homo sapien
45	111.5	4.6	479	11 O8R2V4	O8R2V4 mus musculu

ALIGNMENTS

RESULT 1					
O8TR5		PRELIMINARY:	PRT:	469 AA.	
AC	O8TR5:				
DT	01-JUN-2002 (TREMBLrel. 21, Created)				
DT	01-JUN-2002 (TREMBLrel. 21, Last sequence update)				
DE	01-JUN-2002 (TREMBLrel. 21, Last annotation update)				
DE	Similar to programmed cell death 4 (neoplastic transformation inhibitor).				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE-BRAIN;				
RA	Straussberg R.;				
RL	Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.				
DR	EMBL; BC026104; AAH26104.1; -				
SO	SEQUENCE 469 AA; 51797 MW; 8C72628AFB1330B CRC64;				

Query Match	99.8%	Score 2410;	DB 4;	Length 469;
Best Local Similarity	99.8%	Pred. No. 1.9e-162;		
Matches 469;	Conservative	0;	Mismatches 1;	Indels 0;
				Gaps 0;
OY	1 MDVENEQILNVNPPADPNLSLFSGDENAGTEEVNNEINGNMISASINEARINAKK 60			
DB	1 MDVENEQILNVNPPADPNLSLFSGDENAGTEEVNNEINGNMISASINEARINAKK 60			
OY	61 RLRLKNSRDGSDGSDALRLGGLVPPSPKRLDRSRSGRGLPKKGAGG 120			
DB	61 RLRLKNSRDGSDGSDALRLGGLVPPSPKRLDRSRSGRGLPKKGAGG 120			
OY	121 KGWAGTGGQYVDVGVYKPDNDODDQNCYEVVYVPLDERAFKTLTPIOYFEFGD 180			
DB	121 KGWAGTGGQYVDVGVYKPDNDODDQNCYEVVYVPLDERAFKTLTPIOYFEFGD 180			
OY	181 TNEVAEMRLNLTGEMKSGVVLAVSLALBQKASHREMTSKLSDLGTVASTDIVERKSF 240			
DB	181 TNEVAEMRLNLTGEMKSGVVLAVSLALBQKASHREMTSKLSDLGTVASTDIVERKSF 240			

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Db 181 TNEVAEMRLDNLGEMKSGVPLAVSLAEGKASHREMTSKLLSDLCSTVASTDYDEKSF 240
Qy 241 DKLLKDLPELADTPRAPOLVGOFTIARAVGDIICNTYIDSYKGVDCVOARAALDKATV 300
Db 241 DKLLKDLPELADTPRAPOLVGOFTIARAVGDIICNTYIDSYKGVDCVOARAALDKATV 300
Qy 301 LLSMSGKGRKSDSVMSGGGQSVNHLVKEIDMLKEYLSDISAEHCKLELEVPHPH 360
Db 301 LLSMSGKGRKSDSVMSGGGQSVNHLVKEIDMLKEYLSDISAEHCKLELEVPHPH 360
Qy 361 HELVYEALIMVLESTGESTEFKMIIDLKSLMKSSTITVDQMKRGYERIYNELPIDINDVP 420
Db 361 HELVYEALIMVLESTGESTEFKMIIDLKSLMKSSTITVDQMKRGYERIYNELPIDINDVP 420
Qy 421 HSYSVLERFVEECFOAGIISKOLDLCPGRGKRFRVSEGGGRLEKPEST 469
Db 421 HSYSVLERFVEECFOAGIISKOLDLCPGRGKRFRVSEGGGRLEKPEST 469

RESULT 2
O15501 PRELIMINARY; PRT; 469 AA.
ID O15501
AC O15501:
DT 01-JAN-1998 (TREMblrel. 05, Created)
DT 01-JUN-1998 (TREMblrel. 05, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE Nuclear antigen H731-like protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BLOOD;
RX MEDLINE=98430669; PubMed=9759869;
RA Azzioli L., Zatssepin O., Abebe B., Bennett I.M., Kanakara J.P.,
RA Perussia B.;
RT "Differential transcriptional regulation of CD161 and a novel gene,
RT 197/15a, by IL-2, IL-15, and IL-12 in NK and T cells.";
RL J. Immunol. 161:3493-3500(1998).
DR EMBL: U96628; AAB67706.1;
DR InterPro: IPR003891; IF_eIF4G_MA3.
DR Pfam: PF02847; MA3; 2.
DR SMART: SM00544; MA3; 2.
SQ SEQUENCE 469 AA; 51713 MW; 8A75D7FA36C7496A CRC64;

Query Match 99.0%; Score 2391; DB 4; Length 469;
Best Local Similarity 99.1%; Pred. No. 4.3e-161;
Matches 465; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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Qy 361 HELVYEALIMVLESTGESTEFKMIIDLKSLMKSSTITVDQMKRGYERIYNELPIDINDVP 420
Db 361 HELVYEALIMVLESTGESTEFKMIIDLKSLMKSSTITVDQMKRGYERIYNELPIDINDVP 420
Qy 421 HSYSVLERFVEECFOAGIISKOLDLCPGRGKRFRVSEGGGRLEKPEST 469
Db 421 HSYSVLERFVEECFOAGIISKOLDLCPGRGKRFRVSEGGGRLEKPEST 469

RESULT 3
O61823 PRELIMINARY; PRT; 469 AA.
ID O61823
AC O61823:
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE MA-3 protein.
GN PDCD4 OR MA-3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ICR; TISSUE=THYMUS;
RX MEDLINE=96125207; PubMed=8543179;
RA Shibahara K., Asano M., Ishida Y., Aoki T., Koike T., Honjo T.;
RT "Isolation of a novel mouse gene MA-3 that is induced upon programmed
RT cell death.";
RL Gene 166:297-301(1995).
DR EMBL: D50465; BA09056.1;
DR MGI: MGI:107490; Pdc4.
DR InterPro: IPR003891; IF_eIF4G_MA3.
DR Pfam: PF02847; MA3; 2.
DR SMART: SM00544; MA3; 2.
SQ SEQUENCE 469 AA; 51702 MW; 6883BCE5011692F1 CRC64;

Query Match 97.7%; Score 2361; DB 11; Length 469;
Best Local Similarity 96.6%; Pred. No. 5.7e-159;
Matches 453; Conservative 9; Mismatches 7; Indels 0; Gaps 0;

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RESULT 4
P97296 PRELIMINARY; PRT; 469 AA.

AC P97296;
DT 01-MAY-1997 (TRENBLREL. 03, Created)
DT 01-MAY-1997 (TRENBLREL. 03, Last sequence update)
DT 01-JUN-2002 (TRENBLREL. 21, Last annotation update)
DE Topoisomerase-inhibitor suppressed, complete CDS.
GN PDCD4 OR TIS.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-LYMPHOMA;
RX MEDLINE=97069646; PubMed=8912629;
RA Onishi Y., Kizaki H.;
RT "Molecular cloning of the genes suppressed in RVC lymphoma cells by
topoisomerase inhibitors.";
RL Biochem. Biophys. Res. Commun. 228:7-13(1996).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=98382539; PubMed=9714845;
RA Onishi Y., Hashimoto S., Kizaki H.;
RT "Cloning of the TIS gene suppressed by topoisomerase inhibitors.";
RL Gene 215:453-459(1998).
DR EMBL: D86344; BAA13072.1;
DR EMBL: AB010139; BAA32356.1;
DR EMBL: AB010129; BAA32356.1;
DR EMBL: AB010130; BAA32356.1;
DR EMBL: AB010131; BAA32356.1;
DR EMBL: AB010132; BAA32356.1;
DR EMBL: AB010133; BAA32356.1;
DR EMBL: AB010134; BAA32356.1;
DR EMBL: AB010135; BAA32356.1;
DR EMBL: AB010136; BAA32356.1;
DR EMBL: AB010137; BAA32356.1;
DR EMBL: AB010138; BAA32356.1;
DR MGI: 107490; Pdc4.
DR InterPro: IPR003891; IF_eIF4G_MA3.
DR Pfam: PF02847; MA3; 2.
DR SMART: SM00544; MA3; 2.
KW Isomerase; topoisomerase.
SQ SEQUENCE 469 AA; 51742 MW; FBC5561BA4615D2D CRC64;

Query Match 97.5%; Score 2356; DB 11; Length 469;
Best Local Similarity 96.6%; Pred. No. 1.3e-158;
Matches 453; Conservative 8; Mismatches 8; Indels 0; Gaps 0;

QY 1 MDVNEQILNVNPPADPNLSDSLFSGDEENAGTEEVKNEINGMWISASSINERINAKAK 60
DB 1 MDIENQILNVNPPADPNLSDSLFSGDEENAGTEEVKNEINGMWISASSINERINAKAK 60
QY 61 RRLKNSRSDSGRGDSVSDSGDALRSLGTLVPTSPKGRLLDRSRSGKRGGLPKKGAGC 120
DB 61 RRLKNSRSDSGRGDSVSDSGDALRSLGTLVPTSPKGRLLDRSRSGKRGGLPKKGAGC 120
QY 121 KGVNCTPGQVYDVEVDYKDPYDDQENCYETVYLPDERAFEKTLPPIIQEYFEHGD 180
DB 121 KGVNCTPGQVYDVEVDYKDPYDDQENCYETVYLPDERAFEKTLPPIIQEYFEHGD 180
QY 181 TNEVAEMRLDNLGEMKSGVPYLAVALLEGKASHREMTSKLLSDLCGTVMSTDVESGF 240
DB 181 TNEVAEMRLDNLGEMKSGVPYLAVALLEGKASHREMTSKLLSDLCGTVMSTDVESGF 240
QY 241 DKLKDLPELALDTPRAQOLYGOFTARAVGDIILCNTYIDSYKGTVDVQVAAALDKATV 300
DB 241 DKLKDLPELALDTPRAQOLYGOFTARAVGDIILCNTYIDSYKGTVDVQVAAALDKATV 300
QY 301 LLSMSKGGKRRDSVWGSGGQSVNHLVKEIDMLKEYLLSGDISAEHCKLELEVPFPH 360

|||||
DB 301 LLSMSKGGKRRDSVWGSGGQSVNHLVKEIDMLKEYLLSGDISAEHCKLELEVPFPH 360
QY 361 HELVEAIIWLESTGSEFTKMIIDLKSLMSSTITVDQMKRGERYINEIPDINDVP 420
DB 361 HELVEAIIWLESTGSEFTKMIIDLKSLMSSTITVDQMKRGERYINEIPDINDVP 420
QY 421 HSYSVLEFVEECQAGIISKOLDLCPSSRGKRFVSEGDGRLKPESY 469
DB 421 HSYSVLEFVEECQAGIISKOLDLCPSSRGKRFVSEGDGRLKPESY 469

RESULT 5
O99834 PRELIMINARY; PRT; 458 AA.

AC O99834;
DT 01-MAY-1997 (TRENBLREL. 03, Created)
DT 01-MAY-1997 (TRENBLREL. 03, Last sequence update)
DT 01-JUN-2002 (TRENBLREL. 21, Last annotation update)
DE Nuclear antigen H731.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Matsubashi S., Yoshinaga H., Yatsuki H., Tsugita A., Hori K.;
RT "Isolation of a novel gene from a human cell line with Pr-28 MAb which
recognizes a nuclear antigen involved in the cell cycle.";
RL Res. Commun. Biochem. Cell Mol. Biol. 1:109-120(1997).
DR EMBL: U83908; AAB42218.1;
DR InterPro: IPR003891; IF_eIF4G_MA3.
DR Pfam: PF02847; MA3; 2.
DR SMART: SM00544; MA3; 2.
SQ SEQUENCE 458 AA; 50590 MW; 8D3D850B9D68C1D5 CRC64;

Query Match 96.5%; Score 2332; DB 4; Length 458;
Best Local Similarity 99.6%; Pred. No. 6.3e-157;
Matches 452; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

QY 16 PDLUSDLSFGDEENAGTEEVKNEINGMWISASSINERINAKAKRRLRNSSRSDSGRD 75
DB 5 PDLUSDLSFGDEENAGTEEVKNEINGMWISASSINERINAKAKRRLRNSSRSDSGRD 64
QY 76 SVSDSGDALRSLGTLVPTSPKGRLLDRSRSGKRGGLPKKGAGKGVNCTPGQVYDVEE 135
DB 65 SVSESGDALRSLGTLVPTSPKGRLLDRSRSGKRGGLPKKGAGKGVNCTPGQVYDVEE 124
QY 136 VDYKDPYDDQENCYETVYLPDERAFEKTLPPIIQEYFEHGDINEVAEMLRDLNLGE 195
DB 125 VDYKDPYDDQENCYETVYLPDERAFEKTLPPIIQEYFEHGDINEVAEMLRDLNLGE 184
QY 196 MKSGVPLAVSLALEKASHREMTSKLLSDLCGTVMSTDVESGFKLKDLPELADTP 255
DB 185 MKSGVPLAVSLALEKASHREMTSKLLSDLCGTVMSTDVESGFKLKDLPELADTP 244
QY 256 RAPOLYGOFTARAVGDIILCNTYIDSYKGTVDVQVAAALDKATVLLSMSGKGRKDSV 315
DB 245 RAPOLYGOFTARAVGDIILCNTYIDSYKGTVDVQVAAALDKATVLLSMSGKGRKDSV 304
QY 316 GSGGQGSVNHLVKEIDMLKEYLLSGDISAEHCKLELEVPFPHHELVEAIIWLEST 375
DB 305 GSGGQGSVNHLVKEIDMLKEYLLSGDISAEHCKLELEVPFPHHELVEAIIWLEST 364
QY 376 GESTFMIIDLKSLMSSTITVDQMKRGERYINEIPDINDVPHSYVLEFVEECFO 435
DB 365 GESTFMIIDLKSLMSSTITVDQMKRGERYINEIPDINDVPHSYVLEFVEECFO 424
QY 436 AGIISKOLDLCPSSRGKRFVSEGDGRLKPESY 469
DB 425 AGIISKOLDLCPSSRGKRFVSEGDGRLKPESY 458

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RESULT 6
O9JID1 PRELIMINARY: PRT: 469 AA.
AC 09JID1:
DT 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE Death-upregulated gene.
GN DUG.
OS Rattus norvegicus (Rat.).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA Goke A., Goke R., Milmen A., Goke B., Chen Y.;
RT "UG, a novel homolog of translation initiation factor 4G, regulates
RT cell growth and apoptosis.";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF239739; AAF73961.1;
DR InterPro: IPR003891; IF_eIF4G_MA3.
DR Pfam: PF02847; MA3; 2.
DR SMART: SM00544; MA3; 2.
SQ SEQUENCE 469 AA; 51796 MW; 2B0B007CDB9FDB9 CRC64;

Query Match 95.8%; Score 2314; DB 11; Length 469;
Best Local Similarity 94.7%; Pred. No. 1.2e-155;
Matches 444; Conservative 15; Mismatches 10; Indels 0; Gaps 0;

OY 1 MDVENEOILNVPADPNLSDLSFGDEENAGTEEVKNEINGNMTSASSINEARINAKAK 60
DB 1 MDIENEOILNVPDPDLSDLSFGDEENAGTEEVKNEINGNMTSASSINEARINAKAK 60
OY 61 RLRLKNSRDSGSGDVSNGSDALRSGLTPTSPKGRLLDRSRSGKRGKPKGGAGG 120
DB 61 RLRLKNSRDSGSGDVSNGSEAVRSVAVPTCKGRLLDRSRSGKRGKPKGGAGG 120
OY 121 KGVWGTPGOVYDVEEDVNDPNYDDQENCYETVVLPLDERAFKTLPTIIQEFYEHGD 180
DB 121 KGVWGTPGOVYDVEEDVNDKPNYDDQENCYETVVLPLDERAFKTLPTIIQEFYEHGD 180
OY 181 TNEVAEMRLDLNGEMKSGVPPLAVSLAEGKASHREMTSKLSDLCGTVMSTTVEKSF 240
DB 181 TNEVAEMRLDLNEMKSGVPPLAVSLAEGKASHREMTSKLSDLCGTVMSTTVEKSF 240
OY 241 DKLKDLPELADPRAPOLVGOFIARAVGDLCTYIDSKYGVDCVQARAALDKATV 300
DB 241 DKLKDLPELADPRAPOLVGOFIARAVGDLCTYIDSKYGVDCVQARAALDKATV 300
OY 301 LLSMSKGRKDSVWVGSGGQSVNHLVKEIDMLKEYLLSGDISAEHCKLELEVPHF 360
DB 301 LLSMSKGRKDSVWVGSGGQACHPVYKEIDMLKEYLLSGDISAEHCKLELEVPHF 360
OY 361 HELVEAIIIMVLESTGESEFKMILDLKSLKSSITTVQMKRGYRIINEIPDINLDPV 420
DB 361 HELVEAIIIMVLESTGESEFKMILDLKSLKSSITTVQMKRGYRIINEIPDINLDPV 420
OY 421 HSYSLERFVEECFOAGIISKOLRDLCPGRKRRFVSEGDGRLKPEST 469
DB 421 HSYSLERFVEECFOAGIISKOLRDLCPGRKRRFVSEGDGRLKPEST 469

RESULT 7
O98TX3 PRELIMINARY: PRT: 467 AA.
AC 098TX3:
DT 01-JUN-2001 (TREMblrel. 17, Created)
DT 01-JUN-2001 (TREMblrel. 17, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE Programmed cell death 4 protein.
GN PCO4.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=21214412; PubMed=11313950;
RA Schlichter U., Burk O., Wornberg S., Klempner K.-H.;
RT "The chicken pcd4 gene is regulated by v-Myb.";
RL Oncogene 20:231-239(2001)
DR EMBL: AF21288; AAK09354.1;
DR InterPro: IPR003891; IF_eIF4G_MA3.
DR Pfam: PF02847; MA3; 2.
DR SMART: SM00544; MA3; 2.
SQ SEQUENCE 467 AA; 51707 MW; 361B04FEA47B99EB CRC64;

Query Match 86.0%; Score 2078; DB 13; Length 467;
Best Local Similarity 84.9%; Pred. No. 6.2e-139;
Matches 398; Conservative 39; Mismatches 30; Indels 2; Gaps 2;

OY 1 MDVENEOILNVPADPNLSDLSFGDEENAGTEEVKNEINGNMTSASSINEARINAKAK 60
DB 1 MEIKOHVY-ISTVEVENLSDLSFGDEENAGTEEVKNEINGNMTSASSINEARINAKAK 59
OY 61 RLRLKNSRDSGSGDVSNGSDALRSGLTPTSPKGRLLDRSRSGKRGKPKGGAGG 120
DB 60 RLRLKNSRDSGSGDVSNGSENG-ETQKAGLYVPTSPKGRLLDRSRSGKRGKPKGGAGG 118
OY 121 KGVWGTPGOVYDVEEDVNDPNYDDQENCYETVVLPLDERAFKTLPTIIQEFYEHGD 180
DB 119 KGVWGTPGOVYDVEEDVNDKPNYDDQENCYETVVLPLDERAFKTLPTIIQEFYEHGD 178
OY 181 TNEVAEMRLDLNGEMKSGVPPLAVSLAEGKASHREMTSKLSDLCGTVMSTTVEKSF 240
DB 179 TNEVAEMRLDLNEMKSGVPPLAVSLAEGKASHREMTSKLSDLCGTVMSTTVEKSF 238
OY 241 DKLKDLPELADPRAPOLVGOFIARAVGDLCTYIDSKYGVDCVQARAALDKATV 300
DB 239 DKLKDLPELADPRAPOLVGOFIARAVGDLCTYIDSKYGVDCVQARAALDKATV 298
OY 301 LLSMSKGRKDSVWVGSGGQSVNHLVKEIDMLKEYLLSGDISAEHCKLELEVPHF 360
DB 299 LLSYKGRKIDNVWVGSGGQSVKHLVKEIDMLKEYLLSGDISAEHCKLELEVPHF 358
OY 361 HELVEAIIIMVLESTGESEFKMILDLKSLKSSITTVQMKRGYRIINEIPDINLDPV 420
DB 359 HELVEAIIIMVLESTGESEFKMILDLKSLKSSITTVQMKRGYRIINEIPDINLDPV 418
OY 421 HSYSLERFVEECFOAGIISKOLRDLCPGRKRRFVSEGDGRLKPEST 469
DB 419 HSYSLERFVEECFOAGIISKOLRDLCPGRKRRFVSEGDGRLKPEST 467

RESULT 8
O96944 PRELIMINARY: PRT: 463 AA.
AC 096944:
DT 01-MAY-1999 (TREMblrel. 10, Created)
DT 01-MAY-1999 (TREMblrel. 10, Last sequence update)
DT 01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE MA3 protein.
GN MA3.
OS Suberites domuncula (Sponge).
OC Eukaryota; Metazoa; Porifera; Demospongiae; Tetractinomorpha;
OC Hadromerida; Suberitidae; Suberites.
OX NCBI_TaxID=55567;
RN [1]
RP SEQUENCE FROM N.A.
RA Wagner C., Steffen R., Kozioł C., Batel R., Lacorn M., Steinhart H.,
RA Simat T., Mueller W.B.G.;
RT "Apoptosis in marine sponges: A biomarker for environmental stress
RT (cadmium and bacteria).";
RL Mar. Biol. 131:411-421(1998).
EMBL: Y15421; CAA75614.1;

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DR InterPro: IPR003891; IF_eIF4G_MA3.
 DR Pfam: PF02847; MA3; 2.
 DR SMART: SM00544; MA3; 2.
 SQ SEQUENCE 463 AA; 50765 MW; BE82D8CACE8DEF8 CRC64;
 Query Match 35.6%; Score 859; DB 5; Length 463;
 Best Local Similarity 40.7%; Pred. No. 1.2e-52;
 Matches 200; Conservative 83; Mismatches 152; Indels 56; Gaps 12;

OY 1 MDVNEQLNNPAPDPLDLSLFSGDDEENAGTEVEKNEIKNNMT-----SAS 48
 DB 4 MEVEPQVNGF-----GSKNSPT-----NCHNVOFDTTVKVTMPATS 42
 OY 49 SINEARINAKAKRLRKNSRDGSDGSDALRSGLVPTSP-----KGRLDRS 104
 DB 43 TOPSSRPKHKARRARVPANLIDIGEDERSYST-----TKPPSPSLKMAADKERS 95
 OY 105 RSGKRGRLPKKGGAGKGVWGTGQVYDVEV--DVKDPNVD--DOENCVEYVLPDE 161
 DB 96 RSGR-RGQPKKGGGGKGTGNTIDEMVAEPVTHDTPNDSVEDDATY--LVSPSS 152
 OY 162 RA-----TEKITPLTIOEFEGDINEVEMRLDLNGEKSGVPYLVANSLAEGKASHRE 217
 DB 153 QMSALDEKTAIEIFEKFEYFDHGDQEVASSLELSIKNIKHEVVRIVVTLAEEKAANRE 212
 OY 218 MTSKLSLDLGTVSTTGVSTTVEKSPKLLKDLPELADTPRAPOLVGOFTARAAGDGLCNT 277
 DB 213 KVSIVLLSDLVQVINGREVAKGFLLISQLNDLIDTPDAASVIGNFARCAVDCLPPA 272
 OY 278 YIDSKYGTVDVQARALADKATVLLSMKSGKRKDSVWGSQGGQSVNHLVIMDLKE 337
 DB 273 FVSNHTDVTN-EQIIVALKRAQLLSIKHSIARLDNVWGSGQRPVFLSKMMLLKE 331
 OY 338 YLISGDISEARHCKELEVPFHHELVETAILMVESESTGFKMILLKSLKMSSTT 397
 DB 332 YLSSGDEEATRCRLDEVPFHHELVETAILMVESESTGFKMILLKSLKMSSTT 391
 OY 398 VDOKRGERYIYNEIPDNLVPHSYLSEFVEECPOAGIISKQLRDLCPGRKRRPS 457
 DB 392 TDQNSGIMRVSDMTDVIDIDIPNAVHTLSKFERGAAGAFVSROIABEIPSRGRKRRYS 451
 OY 458 EGDGGRLL-PE 467
 DB 452 EGDGGAIRKSP 462

RESULT 9
 Q9YV91 PRELIMINARY; PRT; 507 AA.
 ID Q9YV91
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE CG10990 protein.
 GN CG10990.
 OS Drosophila melanogaster (Fruit fly)
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 NC NCB1_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RA MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers J.-H.C., Blazey R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abell J.F., Agrawal A., An H.-J., Andrews-Pfankoch C., Baldwin D.,
 RA Bailly R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,

RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
 RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durkin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodok A., Gong F., Correll J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jaitani M., Kalush F., Karpen G.H., Ke Z., Kenison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merulov G., Milshina N.V., Modyarty C., Morris J., Mostrel A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazolo M., Pittman G.S., Pan S., Pollard J., Pui V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Ventler E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Massarman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
 RT "The genome sequence of *Drosophila melanogaster*."
 RL Science 287:2185-2195(2000).
 DR EMBL: AE003493; AAF48312.1;
 DR Flybase: FBgn0030520; CG10990.
 DR InterPro: IPR003891; IF_eIF4G_MA3.
 DR InterPro: IPR00408; Reg_chr-condens.
 DR Pfam: PF02847; MA3; 2.
 DR SMART: SM00544; MA3; 2.
 DR POSITE: PS00626; RC01.2; UNKNOWN.1.
 SQ SEQUENCE 507 AA; 56317 MW; 388E0085427DAD3 CRC64;

Query Match 32.0%; Score 773; DB 5; Length 507;
 Best Local Similarity 35.8%; Pred. No. 1.7e-46;
 Matches 189; Conservative 93; Mismatches 154; Indels 92; Gaps 17;

OY 1 MDVE--NEQILN-----VNPAPDNLSDLSFGDDEENAGTEVEKN-EINGNWTSSASS--- 49
 DB 1 MEVESNNKRTATGGRHFTPPSDSKESSV-----ERELNEIEIAVELNGSGGGSGH 55
 OY 50 -----INEARINAKAKRLRKNSRDGSDVSNS-----GSDALRGL-VP 93
 DB 56 VAKLMAVEDGRILKRAKRLIQKNSGGSANOTNGAAGACAGASVMPGGINRIM 115
 OY 94 SPKGRLL-----DRSRH-SGKRGLPKKGAGKGVWGTG- -QYDVEEYDVKD 140
 DB 116 SPGGYVYVPRKRNKNSRSTIRNGRLPKKGGGGKGVWGLGSESLAEIYE---DEND 171
 OY 141 PNYDD--OENCYETVPLPLDERAFKTLTPILIOEFEGDINEVEMRLDLNGEKMS 198
 DB 172 PNYDECDNRNVELREVITEIRFEFFKLAIEVLEYEYHGPHEVALSFDEILQAPME 231
 OY 199 GYVPLVLALEGKASHREMTSKLSLDLGYWSTTVDKSKDLKLDPELADTPRAP 258
 DB 222 HTSTLVEIAMDHKDSQREMTSVLLSDLVGRVITGDIKGFNMLANLPDLVDPAP 291
 OY 259 QLVGQFIARAAGDGLCNTYIDSYKGYDVCV-----QARAALDKAT 299
 DB 292 IMLGNFMARAAD-----DCIPPKYFAKSGEELRHGLGEHBAQALRRAD 336
 OY 300 VLLSKSGKGRKDSVWGSQGGQSVNHLVETAILMVESESTGFKMILLKSLKMSSTT 359
 DB 337 SLI-YKHWAHLDNWGMGGLRPVKTITMQLLEKLYLSRDAVLAQRALAEVPHY 395
 OY 360 HHELVETAILVLESTGSESTFKMILLKSLKMSSTTVDOKRGERYIYNEIPDNLV 419
 DB 396 HHELVETAILVMTLSOTTERAMCELLKQDLDTCLVLPAGMEGFLRAFDMDVLDV 455

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OY 420 PHSYSLERFVEECFOAGIISQRLDLCPSRGK-RFVSEGDGRUP 466
Db 456 PLAVIILDFEVRGNAGFLTDKIINVPSTRFOAFRR-----GGRRR 498

RESULT 10
O94BRL PRELIMINARY: PRT: 702 AA.
AC O94BRL;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Putative topoisomerase.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC Eucosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,
RA Dale J.M., Gibson H.A., Goldsmith A.D., Jiang P.X., Lee J.M.,
RA Quach H.L., Tang C., Toriumi M., Yu G., Bowser L., Carrincci P.,
RA Chen H., Cheuk R., Hayashizaki Y., Ishida J., Jones T., Kamiya A.,
RA Kaelin-Neumann G., Kawai J., Kim C., Koesema E., Palm B., Lin J.,
RA Meyers M.C., Miranda M., Narusaka M., Nguyen M., Palm C.J.,
RA Sekural T., Satou M., Seki M., Shinn P., Southwick A., Tracy S.E.,
RA Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
RT "Full length cDNA of gene MDC12.16/At5g63190 (GI:10177300).";
RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY039947; AAK64051.1; -.
DR InterPro; IPR003891; IF_eIF4G_MA3.
DR Pfam; PF02847; MA3; 4.
KW Isomerase.
SQ SEQUENCE 702 AA: 77556 MW: 4FB63FB12263C6D9 CRC64:

Query Match 18.1%; Score 438.5; DB 10; Length 702;
Best Local Similarity 31.6%; Pred. No. 1.4e-22;
Matches 130; Conservative 67; Mismatches 172; Indels 43; Gaps 13;

OY 74 GDSVSDSGDALRSLGLTV--PTSPKGRILD-----RRSRGKRGRLPKKGAGKGVWG 125
Db 24 GSLSSPKRHTLPADLNTISPTGKGPVAGIPRNHRIRHSGKHRY-KKEGAGKGTW- 81
OY 126 TFGQVYDVEE---VDVKDPNTD--DDQENCYETVVLPLDERAEKTLPTIIQEFYF 178
Db 82 --GKLLDTDDGSCIDKNPNYDSGEDAYDGLVDSFVSPDLND--YKKSVAIIDEYFST 137
OY 179 GPTNEVAEKLRLDNLGEMSGVPLVLAISLAEKASHRENTSKLLSDLCSTWSTIDYK 238
Db 138 GGVKVAASDLRELGSSEYHPYFTKRLVSNAMDRHREKEKAVLSALYADVILPDQIRD 197
OY 239 SFDKLKDLPELALDTPRAPOLVGOFIARVAGDILCNTYI-----DSYKGVDCVQ 290
Db 198 GTRRLRSVDLADVLDLAVNVLAIFARAIYDEIILPPVFLVSKILPSCGGOVIYV 257
OY 291 ABAALADKATVLLSMKSGKRKDSVWGGGQOQSVNHLVKEIDMLKEYLISGDISAEHC 350
Db 258 AEKSS-----YLSAPHHAELVEKKWG-GSTHTTVEETKKKISIELKEVYNGDYEACRC 310
OY 351 LKELEVPHHHELYVAIIMVLES-TGESTFKIIDLILSLKSSITTVDMKRGYERY 409
Db 311 IRELGVSPFHHEVRAKALVLAADSPTAES--LVTLKLETAEGLISSQWVKGFEFRA 367
OY 410 NEIPDINLDPVPSYSLERFVEECFOAGIISQRLDLCPSRGKRRVSEGD 461
Db 368 ESULDLDLADIPSAKKLFDISIVKRAISGWLDSFKITSDDGK---SSDQG 416

RESULT 11
O9FMK4 PRELIMINARY: PRT: 729 AA.
ID O9FMK4

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AC O9FMK4;
DT 01-MAR-2001 (Tremblrel. 16, Created)
DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Topoisomerase-like protein.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC Eucosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RX MEDLINE=98162728; PubMed=9501997;
RA Nakamura Y., Sato S., Kaneko T., Kotani H., Asamizu E., Miyajima N.,
RA Tabata S.;
RT "Structural analysis of Arabidopsis thaliana chromosome 5. III.
RT Sequence features of the regions of 1,191,918 bp covered by seventeen
RT physically assigned P1 clones."
RL DNA Res. 4:401-414(1997).
DR EMBL; AB008265; BAB10561.1; -.
DR InterPro; IPR003891; IF_eIF4G_MA3.
DR Pfam; PF02847; MA3; 4.
DR SMART; SM00544; MA3; 4.
KW Isomerase.
SQ SEQUENCE 729 AA: 80705 MW: B83717D4372BFC90 CRC64:

Query Match 17.3%; Score 419; DB 10; Length 729;
Best Local Similarity 29.5%; Pred. No. 3.4e-21;
Matches 129; Conservative 67; Mismatches 174; Indels 68; Gaps 13;

OY 74 GDSVSDSGDALRSLGLTV--PTSPKGRILD-----RRSRGKRGRLPKKGAGKGVWG 114
Db 24 GSLSSPKRHTLPADLNTISPTGKGPVAGIPRNHRIRHSGKHRYKVRKLFSEEF 83
OY 115 -----KCGAGKGVWGTGGOVYDVEE---VDVKDPNTD--DDQENCY 152
Db 84 KCVGDIWFTVVAISAGAGKGTW---GKLLDTDDGSCIDKNPNYDSGEDAYDGLVD 140
OY 153 ETVVPLDERAEKTLPTIIQEFYFEGHGTNEVAEMLDNLGEMSGVPLVLAISLEGK 212
Db 141 SPVSDPLND--YKKSVAIIDEYFSTGDKVAASDLRELGSSEYHPYFTKRLVSNAMDRH 198
OY 213 ASHRENTSKLLSDLCSTWSTIDYKSFDKLNDLPRLADTPRAPOLVGOFIARVAGD 272
Db 199 DKREKMAVLSALYADVILPDQIRDFIRLRSVDLADVLDLAVNVLAIFARAIYDE 258
OY 273 ILCNTYI-----DSYKGVDCVQARAALDKATVLLSMKSGKRKDSVWGGGQOQSV 324
Db 259 ILPPVFLVRSKILPESCKGFOYIVTAES-----YLSAPHHAELVEKKWG-GSTHTTV 311
OY 325 NHLVKEIDMLKEYLISGDISAEHCKLEVPFHHELYEALIMVLES-TGESTFKMI 383
Db 312 EETKKKISIELKEVYNGDYEACRCIRELGVSFPFHHEVRAKALVLAADSPTAES--LV 368
OY 384 LDLLSKLSKSSITTVDMKRGYERYINEIPDINLDPVPSYSLERFVEECFOAGIISQRL 443
Db 369 LKLEKTAEGLISSQWVKGFEFRAESLDLADIPSAKKLFDISIVKRAISGWLDSF 428
OY 444 RDLCPSSGRKRRVSEGD 461
Db 429 KITSDDGK---SSDQG 443

RESULT 12
O80548 PRELIMINARY: PRT: 693 AA.
ID O80548
AC O80548;
DT 01-NOV-1998 (Tremblrel. 08, Created)
DT 01-NOV-1998 (Tremblrel. 08, Last sequence update)
DT 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE T22J18.10 protein (Hypothetical 77.2 kDa protein).
GN T22J18.10.

```

OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC Eucosids II; Brassicales; Brassicaceae; Arabidopsis.
 NCBI_TaxID=3702;
 RN
 RP SEQUENCE FROM N.A.
 RA Vysotskaya V.S., Schwartz J.R., Toriumi M., Yu G., Oji O., Kwan A.,
 RA Liu S., Li J., Araujo R., Au M., Brendel V., Buehler E., Conway A.B.,
 RA Conway A.R., Dewar K., Feng J., Kim C., Kurtz D., Li Y., Palm C.J.,
 RA Shinn P., Sun H., Davis R.W., Ecker J.R., Federspiel N.A.,
 RA Theologis A.;
 RT "Arabidopsis thaliana chromosome 1 BAC T22J18 sequence, complete
 RT sequence.";
 RL Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 RN
 RP SEQUENCE FROM N.A.
 RA Yamada K., Liu S.X., Sakano H., Pham P.K., Banh J., Chung M.K.,
 RA Goldsmith A.D., Lee J.M., Quach H.L., Tang C., Toriumi M., Yu G.,
 RA Bowser L., Carninci P., Chen H., Cheuk R., Hayashizaki Y., Ishida J.,
 RA Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Kim C., Koesema E.,
 RA Lam B., Lin J., Meyers M.C., Miranda M., Narusaka M., Nguyen M.,
 RA Palm C.J., Sakurai T., Satou M., Seki M., Shinn P., Southwick A.,
 RA Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
 RT "Full length cDNA of gene T22J18.10 (GI:3287683).";
 RT Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AC003979; AAC2511.1;
 DR EMBL: AY034972; AAK59477.1;
 DR InterPro: IPR003891; IF_eif4g_MA3.
 DR Pfam: PF02847; MA3; 4.
 DR SMART: SM00544; MA3; 4.
 DR Hypothetical protein.
 SQ SEQUENCE 693 AA; 77244 MW; D5EE92BEEC190C15 CRC64;
 Query Match 16.0%; Score 386; DB 10; Length 693;
 Best Local Similarity 28.2%; Pred. No. 6,9e-19;
 Matches 11; Conservative 80; Mismatches 168; Indels 34; Gaps 11;
 QY 77 VSDSGDAL-RSGLTVPST-----PKRLIDRRSRSGKGLPKKGAGKGVWTPGQV 130
 DB 6 LIDSRDPLCISQLKISSSLDPLPQANMAEDLTCSRHSPIKE--GSEETGVE--- 59
 QY 131 YQVEEDVADPNDDQENQVE-TYVLPDEKAFEKTLPPIQVEFHEDTNEVAMLR 189
 DB 60 ---DDDLDPIDPTIEGNSHSDPTSCFDADLSEYKKKAVIEVEFGTNDVSVVNEIK 116
 QY 190 DNLGEMKSGVPLAVSLALEGKASHREMTSKLSDLCGTVMSTDVESKFLKLDPE 249
 DB 117 ELGMAEYRYFYKKLVSMAMDRDKREMAAFLLSTLYADVIDPEYRGRFNKLVSADD 176
 QY 250 LALDTPRAPOLVGQFIARAVGDIICNTYI-----DSYKGTVCQVQRAALDKATVL 301
 DB 177 LSVDDIDAVDVLAVFARAVIDDLPPAPFLKQMKLIPDNSKG---VEVLRKAES--Y 220
 QY 302 LMSKSGKRRKDSVWGGGGQSVNHLVKEIDMLKEILSGDISSEAHCKELEVPFH 361
 DB 231 LATPLAEVVERKMG-GTDNMTAEDVKARINDLKEVMSGDKKEAFRCIKGLKVPFH 289
 QY 362 ELVTEAIIWLESTGSETFKMLDLKSLKSSITVDMQKRGERYIYINIPINDVPH 421
 DB 290 EIVKRALIMAMERRKQV--RLDLDLKEITIEVGLINSTGYTKFSRIIDSLDIDIP 347
 QY 422 SYSLERFVEECFOAG-IISKOLRDICPSGRK 453
 DB 348 ARRIIOSFISKAASEGWLCASSLKSLSADAGEK 380
 RESULT 13
 ID 08W404 PRELIMINARY; PRT; 702 AA.
 AC 08W404;
 DT 01-MAR-2002 (Tremblrel. 20, Created)
 DT 01-MAR-2002 (Tremblrel. 20, last sequence update)

DT 01-JUN-2002 (Tremblrel. 21, last annotation update)
 DE AY4924800/F617.10.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC Eucosids II; Brassicales; Brassicaceae; Arabidopsis.
 NCBI_TaxID=3702;
 RN
 RP SEQUENCE FROM N.A.
 RA Cheuk R., Chen H., Kim C.J., Koesema E., Meyers M.C., Banh J.,
 RA Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y.,
 RA Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G.,
 RA Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M.,
 RA Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T.,
 RA Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K.,
 RA Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
 RA Ecker J.R.;
 RT "Arabidopsis cDNA clones.";
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY062102; AAL32978.1;
 DR InterPro: IPR003891; IF_eif4g_MA3.
 DR Pfam: PF02847; MA3; 4.
 DR SMART: SM00544; MA3; 4.
 SQ SEQUENCE 702 AA; 77435 MW; B7A3BC9548654059 CRC64;
 Query Match 15.3%; Score 369; DB 10; Length 702;
 Best Local Similarity 30.8%; Pred. No. 1.1e-17;
 Matches 108; Conservative 59; Mismatches 154; Indels 30; Gaps 10;
 QY 102 RRSSSGKRGRL-PRKGGAGKGVWG-----TFGQYVDVEVVKPNDDDOE--NCYET 154
 DB 54 KHRSSHGRSIRSRKDDGGGNGMKLIDGDYH---IDPNPNDSGEPELVGAT 109
 QY 155 VVLPDEKAFEKTLPPIQVEFHEDTNEVAMLRDNLGEMKSGVPLAVSLALEGKAS 214
 DB 110 LSDPLDD--YKKAASITINEFTSGDYDVAADILEGSSYHYPIKRLVSMAMDRDK 167
 QY 215 HRENTSKLSDLCGTVMSTDVESKFLKLDPELALDPPRAPOLVGQFIARAVGDI 274
 DB 168 EKEMASVLSALYADVINPQIRDGCVLLLESADPFVDIDAVNVLALFLARAVDIL 227
 QY 275 CNTYID-----SYGTCVQVQRAALDKATVLMSKSGKRRKDSVWGGGGQSVN 326
 DB 228 PPAFLPRAARALPITSRG---YQVQTAES--YLSAAHAEVVERKMG-GQRTVVEE 280
 QY 327 LVEIDMLKEILSGDISSEAHCKELEVPFHHELYEAIWLESTGSETFKMLIDL 386
 DB 281 YKKRIADILWEYETGETYRCRCVRELGVSFHHEVYKRALVTALEN--HAAPVVLK 338
 QY 387 LKSLKSSITVDMQKRGERYIYINIPINDVPHSYSLERFVEECFOAG 437
 DB 339 LNEASENLISSQWVKGFSRLRESLDLALDIRSARTKGLIYPKAVSG 389
 RESULT 14
 ID 09S2X0 PRELIMINARY; PRT; 942 AA.
 AC 09S2X0;
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, last sequence update)
 DT 01-JUN-2002 (Tremblrel. 21, last annotation update)
 DE Hypothetical 104.9 kDa protein.
 GN F617.10 OR AT4G24800.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC Eucosids II; Brassicales; Brassicaceae; Arabidopsis.
 NCBI_TaxID=3702;
 RN
 RP SEQUENCE FROM N.A.
 RA Bevan M., Terry N., Ardiles W., Buyschaert C., Dasevillie R.,
 RA De Clerck R., De Keyser A., Neyt P., Rouze P., Van Den Daele H.,
 RA Villarroel R., Gielens J., Van Montagu M., Bancroft I., Hohneit J.,

